SEQUENCE LISTING

<110> Maliszewski, Charles R. Gayle III, Richard B. Price, Virginia L. Gimpel, Steven D.	
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aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata 15 Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile 15 20 25 30	;6
gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac 20 Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn 35 40 45	14
gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 25 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu 50 55 60	52

tac Tyr	atc Ile	tat Tyr 65	aag Lys	tgg Trp	cca Pro	gca Ala	gaa Glu 70	aag Lys	gag Glu	aat Asn	gac Asp	aca Thr 75	ggc Gly	gtg Val	gtg Val	300
cat His	caa Gln 80	gta Val	gaa Glu	gaa Glu	tgc Cys	agg Arg 85	gtt Val	aaa Lys	ggt Gly	cct Pro	gga Gly 90	atc Ile	tca Ser	aaa Lys	ttt Phe	348
gtt Val 95	cag Gln	aaa Lys	gta Val	aat Asn	gaa Glu 100	ata Ile	ggc Gly	att Ile	tac Tyr	ctg Leu 105	act Thr	gat Asp	tgc Cys	atg Met	gaa Glu 110	396
aga Arg	gct Ala	agg Arg	gaa Glu	gtg Val 115	att Ile	cca Pro	agg Arg	tcc Ser	cag Gln 120	cac His	caa Gln	gag Glu	aca Thr	ccc Pro 125	gtt Val	444
tac Tyr	ctg Leu	gga Gly	gcc Ala 130	acg Thr	gca Ala	ggc Gly	atg Met	cgg Arg 135	ttg Leu	ctc Leu	agg Arg	atg Met	gaa Glu 140	agt Ser	gaa Glu	492
gag Glu	ttg Leu	gca Ala 145	gac Asp	agg Arg	gtt Val	ctg Leu	gat Asp 150	gtg Val	gtg Val	gag Glu	agg Arg	agc Ser 155	ctc Leu	agc Ser	aac Asn	540
tac Tyr	ccc Pro 160	ttt Phe	gac Asp	ttc Phe	cag Gln	ggt Gly 165	gcc Ala	agg Arg	atc Ile	att Ile	act Thr 170	ggc Gly	caa Gln	gag Glu	gaa Glu	588
ggt Gly 175	Ala	tat Tyr	ggc Gly	tgg Trp	att Ile 180	act Thr	atc Ile	aac Asn	tat Tyr	ctg Leu 185	ctg Leu	Gly	aaa Lys	ttc Phe	agt Ser 190	636
cag Gln	aaa Lys	aca Thr	agg Arg	tgg Trp 195	ttc Phe	agc Ser	ata Ile	gtc Val	cca Pro 200	Tyr	gaa Glu	acc Thr	aat Asn	aat Asn 205	cag Gln	684
gaa Glu	acc Thr	ttt Phe	gga Gly 210	Ala	ttg Leu	gac Asp	ctt Leu	ggg Gly 215	Gly	gcc Ala	tct Ser	aca Thr	caa Gln 220	gtc Val	act Thr	732
ttt Phe	gta Val	ccc Pro 225	Glr	. aac . Asn	cag Gln	act Thr	ato Ile 230	: Glu	tcc Ser	cca Pro	gat Asp	aat Asn 235	. Ala	ctg Leu	caa Gln	780
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tgo Cys 255	s Tyr	ggg Gly	g aag 7 Lys	gat S Asp	cag Glr 260	ı Ala	cto Lev	tgg Trp	g cag o Glr	g aaa n Lys 265	s Leu	gco Ala	aag Lys	g gad s Asp	att Ile 270	876
cag Glr	g gtt n Val	gca L Ala	a agt a Sei	aat Asr 275	ı Glu	a att ı Ile	cto E Lei	agg 1 Arg	g gad g As <u>r</u> 280	p Pro	a tgo o Cys	c ttt s Phe	cat His	cct Pro 285	gga Gly	924

tat Tyr	aag Lys	aag Lys	gta Val 290	gtg Val	aac Asn	gta Val	agt Ser	gac Asp 295	ctt Leu	tac Tyr	aag Lys	acc Thr	ccc Pro 300	tgc Cys	acc Thr	972
aag Lys	aga Arg	ttt Phe 305	gag Glu	atg Met	act Thr	ctt Leu	cca Pro 310	ttc Phe	cag Gln	cag Gln	ttt Phe	gaa Glu 315	atc Ile	cag Gln	ggt Gly	1020
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acc Thr 335	agt Ser	tac Tyr	tgc Cys	cct Pro	tac Tyr 340	tcc Ser	cag Gln	tgt Cys	gcc Ala	ttc Phe 345	aat Asn	ggg Gly	att Ile	ttc Phe	ttg Leu 350	1116
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atg Met	aag Lys	ttt Phe	tta Leu 370	aac Asn	ttg Leu	aca Thr	tca Ser	gag Glu 375	aaa Lys	gtc Val	tct Ser	cag Gln	gaa Glu 380	aag Lys	gtg Val	1212
act Thr	gag Glu	atg Met 385	atg Met	aaa Lys	aag Lys	ttc Phe	tgt Cys 390	gct Ala	cag Gln	cct Pro	tgg Trp	gag Glu 395	gag Glu	ata Ile	aaa Lys	1260
aca Thr	tct Ser 400	tac Tyr	gct Ala	gga Gly	gta Val	aag Lys 405	gag Glu	aag Lys	tac Tyr	ctg Leu	agt Ser 410	gaa Glu	tac Tyr	tgc Cys	ttt Phe	1308
tct Ser 415	ggt Gly	acc Thr	tac Tyr	att Ile	ctc Leu 420	tcc Ser	ctc Leu	ctt Leu	ctg Leu	caa Gln 425	ggc Gly	tat Tyr	cat His	ttc Phe	aca Thr 430	1356
gct Ala	gat Asp	tcc Ser	tgg Trp	gag Glu 435	cac His	atc Ile	cat His	ttc Phe	att Ile 440	ggc Gly	aag Lys	atc Ile	cag Gln	ggc Gly 445	agc Ser	1404
gac Asp	gcc Ala	ggc	tgg Trp 450	Thr	ttg Leu	ggc Gly	tac Tyr	atg Met 455	Leu	aac Asn	ctg Leu	acc Thr	aac Asn 460	atg Met	atc Ile	1452
cca Pro	gct Ala	gag Glu 465	Gln	cca Pro	ttg Leu	tcc Ser	aca Thr 470	Pro	ctc Leu	tcc Ser	cac His	tcc Ser 475	Thr	tat Tyr	gtc Val	1500
ttc Phe	ctc Leu 480	Met	gtt Val	cta Leu	ttc Phe	tcc Ser 485	Leu	gtc Val	ctt Leu	ttc Phe	aca Thr 490	Val	gcc Ala	atc Ile	ata Ile	1548
ggc Gly 495	Leu	ctt Leu	atc Ile	ttt Phe	cac His	Lys	cct Pro	tca Ser	tat Tyr	ttc Phe 505	Trp	aaa Lys	gat Asp	atg Met	gta Val 510	1596
tag	-															1599

<210> 2

<211> 510

<212> PRT

<213> Homo sapiens

<400> 2

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Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile Ala Leu 20 25 30

Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
35 40 45

Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile 50 55 60

Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
65 70 75 80

Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln 85 90 95

Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala 100 105 110

Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu 115 120 125

Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu 130 135 140

Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro 145 150 155 160

Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Gly Ala 165 170 175

Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys 180 185 190

Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
195 200 205

Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val 210 215 220

Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg 225 230 235 240

Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr 245 250 255

Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val 260 265 270 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys 275 280 285

Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg 290 295 300

Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly 305 310 315 320

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser 325 330 335

Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro 340 345 350

Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys 355 360 365

Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu 370 375 380

Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser 385 390 395 400

Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly 405 410 415

Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp 420 425 430

Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala 435 440 445

Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala 450 455 460

Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu 465 470 475 480

Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu 485 490 495

Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val 500 505 510

<210> 3

<211> 476

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 3

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys

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- Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly 20 25 30
- Ile Phe Leu Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys 35 40 45
- Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
 50 55 60
- Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln 65 70 75 80
- Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
 85 90 95
- Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala 100 105 110
- Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
 115 120 125
- Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu 130 135 140
- Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro 145 150 155 160
- Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala 165 170 175
- Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys 180 185 190
- Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr 195 200 205
- Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val 210 215 220
- Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg 225 230 235 240
- Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr 245 250 255
- Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val 260 265 270
- Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys 275 280 285
- Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg 290 295 300
- Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly 305 310 315 320

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser 325 330 335

Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro 340 345 350

Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys 355 360 365

Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu 370 375 380

Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser 385 390 395 400

Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly 405 410 415

Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp 420 425 430

Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala 435 440 445

Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala 450 455 460

Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr 465 470 475

<210> 4

<211> 476

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
 construct of human CD39

<220>

<221> VARIANT

<222> (39)

<223> Any amino acid, preferably Cys or Ser

<400> 4

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1 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
20 25 30

Ile Phe Leu Ser Ser Met Xaa Pro Ile Asn Val Ser Ala Ser Thr Leu 35 40 45

Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile 50 55 60

Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala 105 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu 120 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu 135 130 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro 155 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Gly Ala 170 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys 185 180 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr 200 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val 210 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg 235 230 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr 245 255 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val 260 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys 280 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg 295 290 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser 335 325 330 Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro

365

Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys

Pne	370	Asn	Leu	Thr	Ser	G1u 375	Lys	Val	Ser	Gin	380	ьуs	Val	Tnr	GIU	
Met 385	Met	Lys	Lys	Phe	Cys 390	Ala	Gln	Pro	Trp	Glu 395	Glu	Ile	Lys	Thr	Ser 400	
Tyr	Ala	Gly	Val	Lys 405	Glu	Lys	Tyr	Leu	Ser 410	Glu	Tyr	Cys	Phe	Ser 415	Gly	
Thr	Tyr	Ile	Leu 420	Ser	Leu	Leu	Leu	Gln 425	Gly	Tyr	His	Phe	Thr 430	Ala	Asp	
Ser	Trp	Glu 435	His	Ile	His	Phe	Ile 440	Gly	Lys	Ile	Gln	Gly 445	Ser	Asp	Ala	
Gly	Trp 450	Thr	Leu	Gly	Tyr	Met 455	Leu	Asn	Leu	Thr	Asn 460	Met	Ile	Pro	Ala	
Glu 465	Gln	Pro	Leu	Ser	Thr 470	Pro	Leu	Ser	His	Ser 475	Thr					
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att Ile	tac Tyr	ctg Leu	act Thr	gat Asp 85	tgc Cys	atg Met	gaa Glu	aga Arg	gct Ala 90	agg Arg	gaa Glu	gtg Val	att Ile	cca Pro 95	agg Arg	288
											gcc Ala					336
cgg Arg	ttg Leu	ctc Leu 115	agg Arg	atg Met	gaa Glu	agt Ser	gaa Glu 120	gag Glu	ttg Leu	gca Ala	gac Asp	agg Arg 125	gtt Val	ctg Leu	gat Asp	384
gtg Val	gtg Val 130	gag Glu	agg Arg	agc Ser	ctc Leu	agc Ser 135	aac Asn	tac Tyr	ccc Pro	ttt Phe	gac Asp 140	ttc Phe	cag Gln	ggt Gly	gcc Ala	432
agg Arg 145	atc Ile	att Ile	act Thr	ggc Gly	caa Gln 150	gag Glu	gaa Glu	ggt Gly	gcc Ala	tat Tyr 155	ggc Gly	tgg Trp	att Ile	act Thr	atc Ile 160	480
aac Asn	tat Tyr	ctg Leu	ctg Leu	ggc Gly 165	aaa Lys	ttc Phe	agt Ser	cag Gln	aaa Lys 170	aca Thr	agg Arg	tgg Trp	ttc Phe	agc Ser 175	ata Ile	528
gtc Val	cca Pro	tat Tyr	gaa Glu 180	acc Thr	aat Asn	aat Asn	cag Gln	gaa Glu 185	acc Thr	ttt Phe	gga Gly	gct Ala	ttg Leu 190	gac Asp	ctt Leu	576
											caa Gln					624
gag Glu	tcc Ser 210	cca Pro	gat Asp	aat Asn	gct Ala	ctg Leu 215	caa Gln	ttt Phe	cgc Arg	ctc Leu	tat Tyr 220	Gly	aag Lys	gac Asp	tac Tyr	672
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tgg Trp	cag Gln	aaa Lys	ctg Leu	gcc Ala 245	aag Lys	gac Asp	att Ile	cag Gln	gtt Val 250	gca Ala	agt Ser	aat Asn	gaa Glu	att Ile 255	ctc Leu	768
agg Arg	gac Asp	cca Pro	tgc Cys 260	ttt Phe	cat His	cct Pro	gga Gly	tat Tyr 265	aag Lys	aag Lys	gta Val	gtg Val	aac Asn 270	gta Val	agt Ser	816
											gag Glu		Thr			864
		Gln					Gly				tat Tyr 300	Gln				912

													tac Tyr			960
tgt Cys	gcc Ala	ttc Phe	aat Asn	ggg Gly 325	att Ile	ttc Phe	ttg Leu	cca Pro	cca Pro 330	ctc Leu	cag Gln	ggg Gly	gat Asp	ttt Phe 335	Gly	1008
													ttg Leu 350			1056
gag Glu	aaa Lys	gtc Val 355	tct Ser	cag Gln	gaa Glu	aag Lys	gtg Val 360	act Thr	gag Glu	atg Met	atg Met	aaa Lys 365	aag Lys	ttc Phe	tgt Cys	1104
gct Ala	cag Gln 370	cct Pro	tgg Trp	gag Glu	gag Glu	ata Ile 375	aaa Lys	aca Thr	tct Ser	tac Tyr	gct Ala 380	gga Gly	gta Val	aag Lys	gag Glu	1152
aag Lys 385	tac Tyr	ctg Leu	agt Ser	gaa Glu	tac Tyr 390	tgc Cys	ttt Phe	tct Ser	ggt Gly	acc Thr 395	tac Tyr	att Ile	ctc Leu	tcc Ser	ctc Leu 400	1200
													cac His			1248
ttc Phe	att Ile	ggc Gly	aag Lys 420	atc Ile	cag Gln	ggc Gly	agc Ser	gac Asp 425	gcc Ala	ggc Gly	tgg Trp	act Thr	ttg Leu 430	ggc	tac Tyr	1296
atg Met	ctg Leu	aac Asn 435	ctg Leu	acc Thr	aac Asn	atg Met	atc Ile 440	cca Pro	gct Ala	gag Glu	caa Gln	cca Pro 445	ttg Leu	tcc Ser	aca Thr	1344
	ctc Leu 450					taa										1365

<210> 6

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 6

Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Thr Ser Ser Thr 1 5 10 15

Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp 20 25 30

- Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu 35 40 45
- Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val 50 55 60
- Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly 65 70 75 80
- Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg 85 90 95
- Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met 100 105 110
- Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp 115 120 125
- Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala 130 135 140
- Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile 145 150 155 160
- Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile 165 170 175
- Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu 180 185 190
- Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile 195 200 205
- Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr 210 215 220
- Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu 225 230 235 240
- Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu 245 250 255
- Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser 260 265 270
- Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro 275 280 285
- Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His 290 295 300
- Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln 305 310 315 320
- Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly 325 330 335

	Phe	Ser	Ala 340	Phe	Tyr	Phe	Val	Met 345	Lys	Phe	Leu	Asn	Leu 350	Thr	Ser	
Glu	Lys	Val 355	Ser	Gln	Glu	Lys	Val 360	Thr	Glu	Met	Met	Lys 365	Lys	Phe	Cys	
Ala	Gln 370	Pro	Trp	Glu	Glu	Ile 375	Lys	Thr	Ser	Tyr	Ala 380	Gly	Val	Lys	Glu	
Lys 385	Tyr	Leu	Ser	Glu	Tyr 390	Cys	Phe	Ser	Gly	Thr 395	Tyr	Ile	Leu	Ser	Leu 400	
Leu	Leu	Gln	Gly	Tyr 405	His	Phe	Thr	Ala	Asp 410	Ser	Trp	Glu	His	Ile 415	His	
Phe	Ile	Gly	Lys 420	Ile	Gln	Gly	Ser	Asp 425	Ala	Gly	Trp	Thr	Leu 430	Gly	Tyr	
Met	Leu	Asn 435	Leu	Thr	Asn	Met	Ile 440	Pro	Ala	Glu	Gln	Pro 445	Leu	Ser	Thr	
Pro	Leu 450	Ser	His	Ser	Thr											
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<22 <22 <22 <22	3> D c 0> 1> C 2> (onst DS 1)	ruct (143	on o: of 1	f Ar	tifi n CD	39						att	αca	cta	48
<22 <22 <22 <22 <40 atq	3> D c 0> 1> C 2> (0> 7	onst DS 1)	ruct (143 tgg	on of 1 4) atc	f Arnuman	tifi n CD	39 atg	caa	ctc	ctg	tct	tgc	att Ile	gca Ala 15	cta Leu	48
<22 <22 <22 <40 atg Met 1	3> D c 0> 1> C 2> (0> 7 gcc Ala	DS 1)	ruct (143 tgg Trp	on of 1 4) atc Ile 5	f Arr numar gac Asp	tifi n CD agg Arg	atg Met agt	caa Gln gca	ctc Leu 10	ctg Leu act	tct Ser	tgc Cys	Ile tct	Ala 15 aca	Leu aag	48
<22 <22 <22 <40 atg Met 1 agt Ser	3> D c 0> 1> C 2> (0> 7 gcc Ala ctt Leu aca	DS 1) ctg Leu	tgg Trp ctt Leu 20 cta	on of other order of the other of other order order order of other order or	f Arrauman gac Asp aca Thr	agg Arg aac Asn	atg Met agt Ser	caa Gln gca Ala 25	ctc Leu 10 cct Pro	ctg Leu act Thr	tct Ser tca Ser	tgc Cys agt Ser	tct Ser 30	Ala 15 aca Thr	aag Lys	
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cat His	caa Gln	gta Val	gaa Glu	gaa Glu 85	tgc Cys	agg Arg	gtt Val	aaa Lys	ggt Gly 90	cct Pro	gga Gly	atc Ile	tca Ser	aaa Lys 95	ttt Phe	288
gtt Val	cag Gln	aaa Lys	gta Val 100	aat Asn	gaa Glu	ata Ile	ggc	att Ile 105	tac Tyr	ctg Leu	act Thr	gat Asp	tgc Cys 110	atg Met	gaa Glu	336
aga Arg	gct Ala	agg Arg 115	gaa Glu	gtg Val	att Ile	cca Pro	agg Arg 120	tcc Ser	cag Gln	cac His	caa Gln	gag Glu 125	aca Thr	ccc Pro	gtt Val	384
tac Tyr	ctg Leu 130	gga Gly	gcc Ala	acg Thr	gca Ala	ggc Gly 135	atg Met	cgg Arg	ttg Leu	ctc Leu	agg Arg 140	atg Met	gaa Glu	agt Ser	gaa Glu	432
gag Glu 145	ttg Leu	gca Ala	gac Asp	agg Arg	gtt Val 150	ctg Leu	gat Asp	gtg Val	gtg Val	gag Glu 155	agg Arg	agc Ser	ctc Leu	agc Ser	aac Asn 160	480
tac Tyr	ccc Pro	ttt Phe	gac Asp	ttc Phe 165	cag Gln	ggt Gly	gcc Ala	agg Arg	atc Ile 170	att Ile	act Thr	ggc Gly	caa Gln	gag Glu 175	gaa Glu	528
ggt Gly	gcc Ala	tat Tyr	ggc Gly 180	tgg Trp	att Ile	act Thr	atc Ile	aac Asn 185	tat Tyr	ctg Leu	ctg Leu	ggc	aaa Lys 190	ttc Phe	agt Ser	576
cag Gln	aaa Lys	aca Thr 195	agg Arg	tgg Trp	ttc Phe	agc Ser	ata Ile 200	Val	cca Pro	tat Tyr	gaa Glu	acc Thr 205	aat Asn	aat Asn	cag Gln	624
gaa Glu	acc Thr 210	ttt Phe	gga Gly	gct Ala	ttg Leu	gac Asp 215	Leu	ggg	gga Gly	gcc Ala	tct Ser 220	Thr	caa Gln	gtc Val	act Thr	672
ttt Phe 225	gta Val	ccc Pro	caa Gln	aac Asn	cag Gln 230	Thr	ato Ile	gag Glu	tcc Ser	cca Pro 235	gat Asp	aat Asn	gct Ala	ctg Leu	caa Gln 240	720
ttt Phe	cgc Arg	cto Leu	tat Tyr	ggc Gly 245	Lys	gac Asp	tac Tyr	aat Asn	gto Val 250	. Tyr	aca Thr	cat His	ago Ser	Phe 255	ttg Leu	768
tgc Cys	tat Tyr	: Gly	aag Lys 260	Asp	cag Glr	gca Ala	cto Lev	tgg Trp 265	Glr	g aaa 1 Lys	a ctg s Lev	gcc Ala	aag Lys 270	Asp	att Ile	816
cag Gln	gtt Val	gca Ala 275	. Ser	aat Asr	gaa Glu	att Ile	cto Leu 280	ı Arç	gac J Asp	c cca	a tgo Cys	ttt Phe 285	e His	cct Pro	gga Gly	864
tat Tyr	aag Lys 290	Lys	g gta s Val	a gtg L Val	g aac L Asr	gta Val 295	L Sei	gac Asp	c ctt Lei	tad 1 Tyl	c aag r Lys 300	5 Thr	c ccc	c tgo Cys	acc Thr	912

aag aga ttt Lys Arg Phe 305	Glu Met									960
att gga aac Ile Gly Asn										1008
acc agt tac Thr Ser Tyr			Gln Cy							1056
cca cca ctc Pro Pro Leu 355										1104
atg aag ttt Met Lys Phe 370						er Gln				1152
act gag atg Thr Glu Met 385	Met Lys	aag ttc Lys Phe 390	tgt go Cys Al	ct cag la Gln	cct tg Pro Tr 395	gg gag p Glu	gag Glu	ata Ile	aaa Lys 400	1200
aca tct tac Thr Ser Tyr							Tyr			1248
tct ggt acc Ser Gly Thr				eu Leu						1296
gct gat tcc Ala Asp Ser 435										1344
gac gcc ggc Asp Ala Gly 450						u Thr				1392
cca gct gag Pro Ala Glu 465	Gln Pro I			o Leu				taa		1437
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Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys 20 25 30

Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn 35 40 45

Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu 50 55 60

Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val 65 70 75 80

His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe 85 90 95

Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu 100 105 110

Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val 115 120 125

Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu 130 135 140

Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn 145 150 155 160

Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu 165 170 175

Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser 180 185 190

Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln 195 200 205

Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr 210 215 220

Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln 225 230 235 240

Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu 245 250 255

Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile 260 265 270

Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly 275 280 285

Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr 290 295 300

Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly 305 310 315 320

Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn 325 330 335

Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu 340 345 350

Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val 355 360 365

Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val 370 375 380

Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys 385 390 395 400

Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe 405 410 415

Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gly Tyr His Phe Thr 420 425 430

Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser 435 440 445

Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile 450 455 460

Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr 465 470 475

<210> 9

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<400> 9

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser 20

<210> 10

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 peptide

<400> 10

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Asp Tyr Lys Asp Asp Asp Lys
<210> 11
<211> 43
<212> PRT
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Fusion
      construct of human CD39
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Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys
<210> 12
<211> 29
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Fusion
      construct of human CD39
<400> 12
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
                                      10
Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys
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<210> 13
<211> 31
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Fusion
       construct of human CD39
<400> 13
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Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Ser Thr Gln Asn Lys
              20
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(213) Altiticial Sequence	
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tgtccacacc tctctcccac gagcccc	87
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aggttcagca tgtagcccaa agtccag	87
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<220> <221> CDS <222> (42)(737)	
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gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc gag ggc Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly 10 15 20	104
gcg ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 25 30 35	152
atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His 40 45 50	200

gaa gac Glu Asp 55															248
cat aat His Asn 70															296
cgg gtg Arg Val															344
aag gac Lys Asp															392
cag aaa Gln Lys															440
tac acc Tyr Thr 135															488
ctg acc Leu Thr 150															536
tgg gag Trp Glu															584
gtg ctg Val Leu															632
gac aag Asp Lys															680
cat gag His Glu 215	Ala	ctg Leu	cac His	aac Asn	cac His 220	tac Tyr	acg Thr	cag Gln	aag Lys	agc Ser 225	ctc Leu	tcc Ser	ctg Leu	tct Ser	728
ccg ggt Pro Gly 230		tga													740
<210> 1 <211> 2 <212> P <213> H	32 RT	sapi	ens												
<400> 1 Glu Pro		Ser	Cys 5	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro 15	Ala	

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val 55 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln 85 Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala 105 Leu Pro Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr 135 130 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg 150 His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr 180 185 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe 200 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys 210 215 Ser Leu Ser Leu Ser Pro Gly Lys 230 <210> 18 <211> 18 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: Synthetic oligonucleotide <400> 18 ctttccatcc tgagcaac

<210> 19 <211> 36

18

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<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide
<400> 19
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aaaaaactag tcagaacaaa gctttgccag aaaacg
<210> 20
<211> 24
<212> PRT
<213> Mus sp.
<400> 20
Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
                                      10
Leu Val Leu Leu Pro Val Thr Ser
             20
<210> 21
<211> 46
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide
<400> 21
                                                                    46
ctagttctgg agactacaaa gatgacgatg acaaaaccca gaacaa
<210> 22
<211> 46
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
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<400> 22
                                                                    46
agctttgttc tgggttttgt catcgtcatc tttgtagtct ccagaa
<210> 23
<211> 89
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic
      oligonucleotide
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	89
tgtccacacc tctctcccac tccacctaa	0,5
<210> 24 <211> 89 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide	
<400> 24 ggccttaggt ggagtgggag agaggtgtgg acaatggttg ctcagctggg atcatgttgg	60
tcaggttcag catgtagccc aaagtccag	89
<210> 25 <211> 1464 <212> DNA <213> Artificial Sequence	
<220> <221> CDS <222> (1)(1461)	
<220> <223> Description of Artificial Sequence: Fusion construct of human CD39	
<pre><400> 25 atg gcc ctg tgg atc gac agg atg caa ctc ctg tct tgc att gca cta Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu 1 5 10 15</pre>	48
agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys 20 25 30	96
aaa aca cag cta act agt tca gga gac tac aaa gat gac gat gac aaa Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Asp Lys 35 40 45	144
acc cag aac aaa gca ttg cca gaa aac gtt aag tat ggg att gtg ctg Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu 50 55 60	192
gat gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala	240

gaa Glu	aag Lys	gag Glu	aat Asn	gac Asp 85	aca Thr	ggc Gly	gtg Val	gtg Val	cat His 90	caa Gln	gta Val	gaa Glu	gaa Glu	tgc Cys 95	agg Arg	288
gtt Val	aaa Lys	ggt Gly	cct Pro 100	gga Gly	atc Ile	tca Ser	aaa Lys	ttt Phe 105	gtt Val	cag Gln	aaa Lys	gta Val	aat Asn 110	gaa Glu	ata Ile	336
ggc Gly	att Ile	tac Tyr 115	ctg Leu	act Thr	gat Asp	tgc Cys	atg Met 120	gaa Glu	aga Arg	gct Ala	agg Arg	gaa Glu 125	gtg Val	att Ile	cca Pro	384
agg Arg	tcc Ser 130	cag Gln	cac His	caa Gln	gag Glu	aca Thr 135	ccc Pro	gtt Val	tac Tyr	ctg Leu	gga Gly 140	gcc Ala	acg Thr	gca Ala	ggc Gly	432
atg Met 145	cgg Arg	ttg Leu	ctc Leu	agg Arg	atg Met 150	gaa Glu	agt Ser	gaa Glu	gag Glu	ttg Leu 155	gca Ala	gac Asp	agg Arg	gtt Val	ctg Leu 160	480
gat Asp	gtg Val	gtg Val	gag Glu	agg Arg 165	agc Ser	ctc Leu	agc Ser	aac Asn	tac Tyr 170	ccc Pro	ttt Phe	gac Asp	ttc Phe	cag Gln 175	ggt Gly	528
gcc Ala	agg Arg	atc Ile	att Ile 180	act Thr	ggc Gly	caa Gln	gag Glu	gaa Glu 185	ggt Gly	gcc Ala	tat Tyr	ggc	tgg Trp 190	att Ile	act Thr	576
atc Ile	aac Asn	tat Tyr 195	ctg Leu	ctg Leu	ggc	aaa Lys	ttc Phe 200	agt Ser	cag Gln	aaa Lys	aca Thr	agg Arg 205	tgg Trp	ttc Phe	agc [.] Ser	624
ata Ile	gtc Val 210	Pro	tat Tyr	gaa Glu	acc Thr	aat Asn 215	Asn	cag Gln	gaa Glu	acc Thr	ttt Phe 220	Gly	gct Ala	ttg Leu	gac Asp	672
ctt Leu 225	Gly	gga Gly	gcc Ala	tct Ser	aca Thr 230	Gln	gtc Val	act Thr	ttt Phe	gta Val 235	Pro	caa Gln	aac Asn	cag Gln	act Thr 240	720
atc Ile	gag Glu	tcc Ser	cca Pro	gat Asp 245	Asn	gct Alæ	ctg Leu	caa Gln	ttt Phe 250	e Arg	cto Leu	tatı Tyr	. Gly	e aag Lys 255	gac Asp	768
tac Tyr	aat Asr	gto Val	tao Tyr 260	Thr	cat His	ago Ser	ttc Phe	ttg Lev 265	і Суя	tat Tyr	ggg Gly	ı aaç ⁄ Lys	gat Asp 270	GIT.	gca Ala	816
cto Lev	tgg ı Trp	g cag Glr 275	і Гуз	a cto s Lev	gco Ala	c aag a Lys	gac S Asp 280	o Il∈	caç e Glr	g gtt n Val	gca L Ala	a agt a Ser 285	Asr	gaa Glu	att ı Ile	864
cto Lev	agg 1 Arg 290	g Asg	c cca p Pro	a tgo	ttt Phe	cat His 295	s Pro	gga Gly	a tat / Ty:	t aag	g aag E Lys 300	s Val	a gtg L Val	g aad L Asr	gta 1 Val	912

agt g Ser A 305				_			_		_	_			_			960
cca t Pro P		_	_		_		_								_	1008
cat c His G		_		_						_		_				1056
cag t Gln C	Zys	-						_				_		-		1104
Gly A 3																1152
tca g Ser G 385	-		-		_	_	_				_	_		_		1200
tgt g Cys A		_										_		_	-	1248
gag a Glu L	_		_	_	_		_									1296
ctc c Leu L	Leu	_							_	_			-			1344
cat t His P				_		_		_	_	_				_		1392
tac a Tyr M 465	_	_		_			_			_				-		1440
aca c							taa									1464

<210> 26

<211> 487

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct of human CD39

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
20 25 30

Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Asp Lys 35 40 45

Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu 50 60

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala 65 70 75 80

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg 85 90 95

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile 100 105 110

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro 115 120 125

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly 130 135 140

Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu 145 150 155 160

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
165 170 175

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr 180 185 190

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser 195 200 205

Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp 210 215 220

Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr 225 230 235 240

Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp 245 250 255

Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala 260 265 270

Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile 275 280 285

Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val 290 295 300

Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu 305 310 315

Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys 325 330 335

His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser 340 345 350

Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe 355 360 365

Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr 370 380

Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe 385 390 395 400

Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys 405 410 415

Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser 420 425 430

Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile 435 440 445

His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly 450 455 460

Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser 465 470 475 480

Thr Pro Leu Ser His Ser Thr 485

<210> 27

<211> 464

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
 construct of human CD39

<400> 27

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys Ala Leu Pro $20 \\ 25 \\ 30$

Glu Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr $35 \hspace{1cm} 40 \hspace{1cm} 45$

Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly 50 60

Val Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser 65 Lys Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr 105 Pro Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu 135 Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln 155 160 145 150 Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys 170 Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn 185 Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln 200 195 Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala 215 Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser 240 230 235 Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys 250 Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His 265 Pro Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro 275 Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile 295 Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu 305 Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile 325 330

Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr 340 345 350

Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu

360

355

Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu 370 375 380

Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr 385 390 395 400

Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gly Tyr His
405
410
415

Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln 420 425 430

Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn 435 440 445

Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr 450 455 460

<210> 28

<211> 474

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
 construct of human CD39

<400> 28

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Thr Lys Lys Thr Gln Leu 20 25 30

Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly 35 40 45

Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys
50 55 60

Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu 65 70 75 80

Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val 85 90 95

Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu 100 105 110

Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala 115 120 125

Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp 130 135 140 Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp 155 145 Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly 165 Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg 185 Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly 200 Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln 220 215 Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr 240 230 225 Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys 245 Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser 265 Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val 275 280 Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu 295 Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr 315 320 305 Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys 330 325 Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln 345 Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu 355 Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met 375 Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala 395 390 385 Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr 405 Ile Leu Ser Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp 425 Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp 435 440

Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln 450 455 460

Pro Leu Ser Thr Pro Leu Ser His Ser Thr 465 470

<210> 29

<211> 473

<212> PRT

<213> Artificial Sequence

<220>

<400> 29

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ser Thr Lys Lys Thr Gln Leu Thr 20 25 30

Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile 35 40 45

Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp
50 55 60

Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu 65 70 75 80

Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn 85 90 95

Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val 100 105 110

Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr
115 120 125

Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg 130 135 140

Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe 145 150 155 160

Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp 165 170 175

Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp
180 185 190

Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala 195 200 205

Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn 210 215 220

Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly 225 230 235 240

Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp 245 250 255

Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn 260 265 270

Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val 275 280 285

Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met 290 295 300

Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln 305 310 315 320

Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro 325 330 335

Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly 340 345 350

Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn 355 360 365

Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys 370 375 380

Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly 385 390 395 400

Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile 405 410 415

Leu Ser Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu 420 425 430

His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr 435 440 445

Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro 450 455 460

Leu Ser Thr Pro Leu Ser His Ser Thr
465 470

<210> 30

<211> 463

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
 construct of human CD39

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Gly Ser Thr Gly Ala Pro Thr Ser Thr Gln Asn Lys Ala Leu Pro Glu 20 25 30

Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser 35 40 45

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val
50 55 60

Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys 65 70 75 80

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met 85 90 95

Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro 100 105 110

Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser 115 120 125

Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser 130 135 140

Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu 145 150 155 160

Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe 165 170 175

Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn 180 185 190

Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val 195 200 205

Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu 210 215 220

Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe 225 230 235 240

Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp 245 250 255

Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro 260 265 270

Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys 275 280 285

Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln 290 295 300

Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe 305 310 315 320

Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe 325 330 335

Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe 340 345 350

Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys 355 360 365

Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile 370 375 380

Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys 385 390 395 400

Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gly Tyr His Phe 405 410 415

Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly 420 425 430

Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met 435 440 445

Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr 450 455 460

<210> 31

<211> 58

<212> PRT

<213> Homo sapiens

<400> 31

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys

1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
20 25 30

Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu 35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr 50 55